

Overexpression of cyclooxygenase-2 (COX-2) in the mouse urinary bladder induces the expression of immune and cell proliferation related genes

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ABSTRACT

Bladder cancer is a common malignancy. Numerous studies have demonstrated that increased expression of cyclooxygenase enzyme 2 (COX-2), which catalyzes the synthesis of prostaglandins (PGs), is associated with the development and progression of certain type of cancers, including bladder cancer. However, the exact role of COX-2/PGs play in bladder carcinogenesis remains unknown. We have recently developed a transgenic mouse model which overexpresses COX-2 under the promoter of the bladder cancer specific promoter, the BK5.COX2 mice develop high incidence of bladder transitional cell hyperplasia (TCH) and a relative lower incidence of bladder papilloma. We then conducted a microarray gene analysis to determine the effects of COX-2 overexpression on the regulation of gene expression profile in bladder carcinogenesis. Analysis of gene array data by t-test ($p < 0.05$) revealed 70 of the upregulated genes and 60 of the downregulated genes had expression changed by 2-fold or more in transgenic compared to wild-type bladders. Gene set analysis using Expression Analysis Systematic Explorer software revealed that genes associated with Immune/Stress response, cell cycle, and cell growth and proliferation were significantly overrepresented in the top 100 upregulated genes. Relevant downregulated genes included three TGF beta related genes (Tgfb2, Tgfb3, Tgfb1), and the anti-angiogenic gene thrombospondin 2 (Thbs2). We further demonstrated that the growth factor, epiregulin, is the most highly induced gene among the genes validated by real-time PCR. The results of gene expression analysis indicate that the initial response of the mouse bladder to elevated COX-2 expression includes mounting an inflammatory response and inducing cell proliferation. Future studies will focus on determining the role of the immune response in bladder carcinogenesis, the role of epiregulin in bladder transitional epithelium, the role of epiregulin and the downstream signaling molecules in bladder carcinogenesis will also be determined. This study was supported by grants CA901865 and CA100140 from the National Cancer Institute.

METHODS

Materials. Polyclonal anti-human COVID-19, COVID-2 antibodies and PGE₂, EAE kit were from Cayman Chemical (Ann Arbor, MI). anti-Rabbit HRP-linked IgG and HRP-conjugated anti-mouse antibody were from Cell Signaling (Beverly, MA). Polyclonal bovine anti-human IL-6 antibody was from R&D Systems (Minneapolis, MN). Recombinant human IL-6 (Carlsbad, CA), cRNeasy Mini RNA extraction kit was purchased from Qiagen (Valencia, CA). COVID-19, COVID-2, epigenagin, IFN- γ , IGFBR3, TGF β , TGF β 2 TGFB3 and GAPDH primers were synthesized by Integrated DNA Technologies Inc. from ApPLIED Biosystems (Foster City, CA) as was the TaqMan® Universal Master Mix.

Animal Maintenance. Wild-type FVB mice and BKSC02 transgenic mice (FVB background) were housed at the University of Illinois at Chicago (UIC) animal facility under One State University (OSU) under all artificial daylight rhythms and fed chow and water *ad libitum*. All procedures followed were approved by the Institutional Animal Care and Use Committee. Only female wild-type and transgenic mice were used for these studies.

Real-time PCR. Total RNA from age matched wild-type and BKSC02 mice was isolated using Trizol reagent (Life Technologies, Gaithersburg, MD). Total RNA was isolated in three pooled wild-type mouse bladders was used as a calibration sample. Total RNA was quantified using a NanoDrop spectrophotometer (ThermoFisher Scientific, Waltham, MA). PCR shared efficiency. Total RNA (10 ng) was reverse transcribed with iScript cDNA synthesis kit (Bio-Rad, Richmond, CA). Real-time PCR was performed on a 1:10 dilution of the cDNA, using Taqman gene expression assays (Applied Biosystems, Foster City, CA) and TaqMan Gene Expression Cycle IC real-time PCR detection system (Bio-Rad). GAPDH was used as the reference gene.

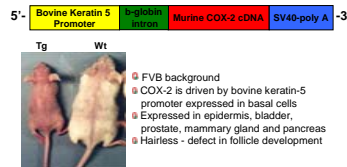
AflymeR1 microarray and transgenic mice. AfflymeR1 bladder tissues were excised from 10 wk old wild-type and BKS. COX-2 transgenic mice (5 mice/group). Total RNA were extracted by TRIzol reagent and then purified by RNeasy kit. The AfflymeR1 microchip analysis was performed by the Microarray Core Facility at the Columbus Children's Hospital Medical Center. Ten Mouse 430 GeneChips (AfflymeR1, Santa Clara, CA) were used; one chip for each sample. GeneChip MicroArray Suite was used to scan and quantitate the data. The raw data were then normalized by the Robust Multi-array Analysis (RMA) sequentially to standardize, normalization, filtering, and functional classification. Differentially expressed genes in BKS COX2 mice versus wild-type mice were identified by log₂-differences and by t-test. The results were further analyzed using Expression Analysis Systematic Explorer (EASE; NIH) with the Benjamin false discovery

Tissue Preparation and Histological Analysis. Urinary bladders were excised and fixed in 10% Formalin. The fixed bladders were then bisected longitudinally through the urethral opening and positioned with the cut faces oriented in the same direction for paraffin embedding. Four-micron sections were stained with hematoxylin and eosin (H&E) by standard protocols. Immunohistochemical staining was carried out using modified ABC techniques. Primary antibody dilution for COX-2 was 1:2000 overnight at 4°C. Species appropriate biotinylated secondary antibodies were used at 1:200 for 2 hours at RT followed by ABC-HRP or SA-HRP treatment for 30 minutes at RT. Slides were developed with DAB for approximately five minutes. Mouse Ki-67 staining was performed by the

Immunoblot Analysis. Immunoblot analysis of COX-2, COX-1 and beta-actin were carried out according to the antibody manufacturer's instructions. Cell lysates from mouse was deferens was used as positive control.

Statistical Analysis. All data were analyzed by SPSS software. Values are means \pm SD. Statistical significance ($p < 0.05$) was determined by t-test.

BK5.COX2 MODEL



OBJECTIVES

- To determine the effect of COX-2 overexpression on the gene expression profile in bladder epithelium.
- To explore potential mechanisms by which COX-2 can influence urinary bladder carcinogenesis.

INTRODUCTION

Bladder cancer represents an important health concern. The identification of new molecular targets for bladder cancer prevention and therapy is a potential means to reduce the development and progression of this disease. Numerous studies have demonstrated that COX-2 is overexpressed in TCC of human urinary bladder [1-4]. The degree of COX-2 expression is significantly correlated with the tumor grade and depth of invasion (T stage) of COX [5-7]. Increased COX-2 expression has also been reported in rat and canine models of bladder cancer [8,9]. A case-control study involving 154 incident bladder cancer cases and an age-matched control group found that the use of COX-2 inhibitors (users have an almost 20% decreased risk for urinary bladder cancer [10]. A number of studies have demonstrated that NSAIDs are able to inhibit the growth of bladder cancer cells *in vitro* [11-14]. In addition, COX inhibitors also induced remission of chemically induced bladder tumors in rodents [15-16], naturally occurring invasive bladder tumors in dogs [17-18], and bladder carcinoma in an orthotopic mouse model [19]. We have recently demonstrated that forced expression of COX-2, under the control of a keratin 5 (K5) promoter, is sufficient to cause urinary bladder transitional cell hyperplasia (TCH), which progresses to TCC in a small percentage of transgenic mice [20]. The level of COX-2 expression, E_2 product, and major product of COX-2, PGI_2 , was significantly increased in the bladder of BKS.COX-2 mice. PGE₂ has also been reported to be elevated in patients with bladder cancer [4,21].

The above studies suggest that there is a strong association between COX-2, prostaglandin synthesis and the development and progression of urinary bladder cancer. However, the exact role and mechanisms of COX-2 overexpression during bladder carcinogenesis have not been well defined. To determine the molecular events elicited by COX-2 overexpression during the early stage of bladder carcinogenesis (before the onset of substantial tumor growth), we conducted DNA microarray expression analysis on urinary bladders from 10 wk old wild-type and COX-2BKS.5COX2 transgenic mice. Our study is innovative in that we were able to study gene expression changes that were due solely to the overexpression of COX-2 in the bladder tissue of a novel transgenic mouse model. This model may serve as a potentially useful model to study the etiology and prevention of human urinary bladder cancer.

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RESULTS

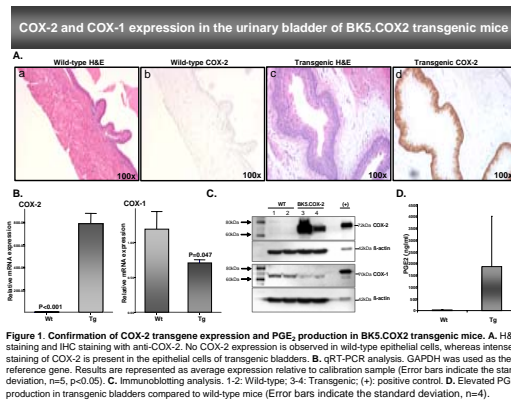


Figure 1. Confirmation of COX-2 transgene expression and PGE₂ production in BK5.COX2 transgenic mice. A. H&E staining and IHC staining with anti-COX-2. No COX-2 expression is observed in wild-type epithelial cells, whereas intense staining of COX-2 is present in the epithelial cells of transgenic bladders. B. qRT-PCR analysis. GAPDH was used as the reference gene. Results are represented as average expression relative to calibration sample (Error bars indicate the standard deviation, n=5, p<0.05). C. Immunoblotting analysis. 1-2: Wild-type; 3-4: Transgenic; (+): positive control. D. Elevated PGE₂ production in transgenic bladders compared to wild-type mice (Error bars indicate the standard deviation, n=4).

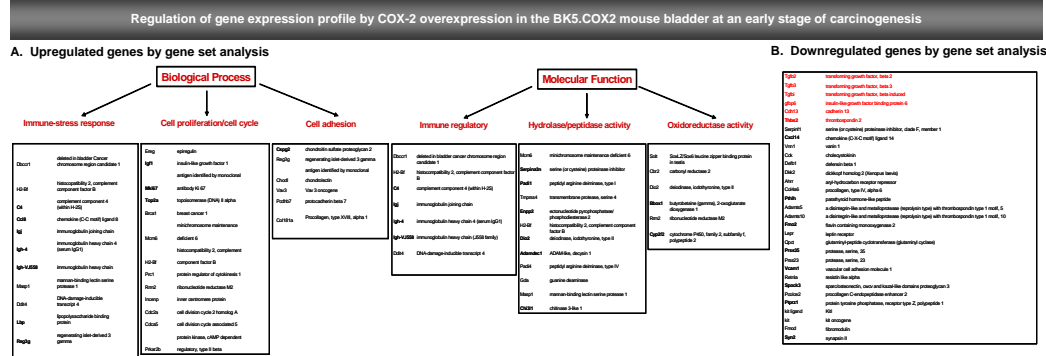


Figure 3. Affirmar Microarray analysis of gene regulation in 10 wk old BK5.COX2 mice (n=5) compared to the wild-types (n=5). A. Upregulated genes. B. Downregulated genes. Analysis of gene array data by t-test ($p < 0.05$) revealed that 2270 genes were upregulated and 1740 genes were downregulated in COX2 mice compared to wild-type mice. Seventy upregulated genes and sixty downregulated genes had expression changed by 2-fold or more (bold text) in transcription compared to wild-type bladders. Gene set analysis of the array data using Expression Analysis System Explorer (EASE; NIH) software determined that genes associated with Immune/Stress Response, Cell Cycle/Proliferation process, and Extracellular Matrix remodeling were upregulated (A) (EASE-0.05; Benjamini-c1.0); relevant downregulated genes include TGF-beta related genes (Tgfb2, Tgfb3, Tgfbp1), and the anti-angiogenic gene thrombospondin 2 (Thbs2) (Panel B, red text).

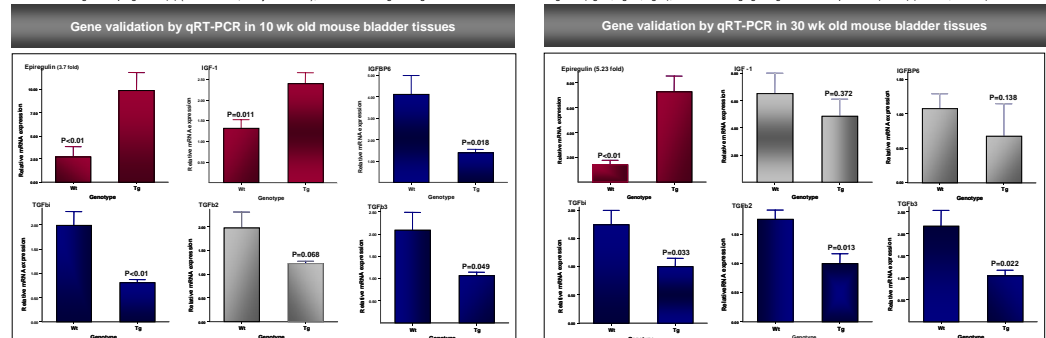


Figure 4 qRT-PCR validation of six genes of interest that were significantly upregulated in 10 wk old BK5/COS2 transgenic mice by Gene Array analysis. Note that epigruin is the most significantly upregulated gene (increased in BK5/COS2 by 3.7 fold, $p < 0.01$). GAPDH was used as the reference gene. Results are represented as average expression relative to GAPDH \pm standard error of the mean. Bars are color coded by color: red, significantly upregulated genes; blue, significantly downregulated genes; grey, no significance ($p < 0.05$).

Ki67 staining is increased in BK5.COX2

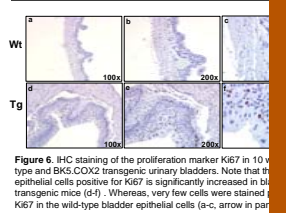


Figure 6. IHC staining of the proliferation marker Ki67 in 10 v type and BK5.COX2 transgenic urinary bladders. Note that the epithelial cells positive for Ki67 is significantly increased in bk transgenic mice (d-f). Whereas, very few cells were stained for Ki67 in the wild-type bladder epithelial cells (a-c, arrow in panel

CONCLUSIONS

- COX-2 overexpression induces the release of genes involved in immune/stress, antiangiogenic, proliferation/cell cycle extracellular matrix remodeling events initiating responses.
- The growth factor, epiregulin, is the most significantly upregulated gene as validated by qRT-PCR.
- The expression of epiregulin and the TGF- β signaling pathway were consistently deregulated in the progression of urinary bladder carcinogenesis.
- BK5, COX2 may serve as a mouse model for human bladder carcinogenesis.
- Biomarkers of COX-2 overexpression may be useful in future translational chemoprevention studies focusing on bladder cancer.

FUTURE DIRECTION

- Determine the presence and level of prostaglandins and their respective receptors
- Determine the role of epiregulin, downstream signaling molecules in carcinogenesis.
- Examine the interaction between COX-2 and TGF-beta signaling pathways in carcinogenesis.
- Explore the role of the immune response in regulating the hyperplastic response in bladder transitional epithelium.

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